Plea se cancel the present "SEQUENCE LISTING", submitted on compact disc in accordance with 37 C.F.R. §1.821(c), and insert therefor the accompanying Substitute Sequence Listing submitted on compact disc in accordance with 37 C.F.R. §1.821(c).

REMARKS

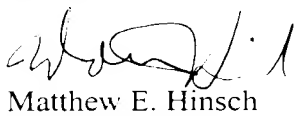
Please replace the two copies of the written Sequence Listing, submitted on compact disc in accordance with 37 C.F.R. §1.821(c) filed November 15, 2000, with the two substitute copies of the written Sequence Listing submitted herewith on compact disc in accordance with 37 C.F.R. §1.821(c). The required duplicate copies of the written form on compact disc are labeled "Copy 1 of 3" and "Copy 2 of 3". The computer readable form of the Substitute Sequence Listing is also submitted on compact disc, labeled "Copy 3 of 3".

Each compact disc is formatted for IBM-PC, MS-Windows 98. Each disc contains one file: -140.APP, 582,722 bytes, created on April 26, 2001 containing the above named sequences, SEQ ID NOS:1-3683. The duplicate copies of the written form on compact disc and the computer readable form of the Substitute Sequence Listing on compact disc are identical, *i.e.*, "Copy 1 of 3" and "Copy 2 of 3" of the compact discs are identical, and the sequence information recorded in computer readable form on compact disc, *i.e.*, "Copy 3 of 3", is identical to the written (on compact disc) Substitute Sequence Listing.

In order to expedite prosecution, Applicants have included the theoretical peptides (SEQ ID NOS:3682 and 3683) in the Substitute Sequence Listing as requested by the Examiner. Applicants note that each amino acid position TABLE III independently defines preferred and deleterious residues; there is no basis in the specification to assume otherwise. Thus, a peptide with a preferred residue at position 3, for example, need not have another preferred residue at position 4. The Examiner's request to include a specific sequence for the amino acid residues set forth at positions 1-9 for DR7 from TABLE III, page 99, in the Substitute Sequence Listing is therefore directed to a purely theoretical peptide that would comprise all of the preferred residues (SEQ ID NO:3682) or all of the deleterious residues (SEQ ID NO:3683) at secondary positions. These amendments to the specification add no new matter.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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MEH:dmw

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 5 of page 2 has been amended as follows:

The Sequence Listing written in file -140.APP ~~140.00 FINAL SEQ LIST.TXT~~, 582,722 ~~582,256~~ bytes, created on April 26, 2001 ~~November 14, 2000~~ on two identical copies of compact discs for Application No: 09/357,737, Sette *et al.*, INDUCING CELLULAR RESPONSES TO HEPATITIS C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS, is hereby incorporated-by-reference.

Paragraph beginning at line 5 of page 76 has been amended as follows:

In summary, on the basis of the data presented in the above examples, 26 CTL candidate peptide epitopes derived from conserved regions of the HCV virus have been identified (Table XXXVIa). These include twelve HLA-A2 supermotif-bearing epitopes, eight HLA-A3 supermotif-bearing epitopes, and one HLA-B7 supermotif-bearing epitope, each capable of binding to multiple A2-, A3-, or B7-supertype molecules, and immunogenic in HLA transgenic mice or antigenic for human PBL (with the exception of peptide 29.0035/1260.04). Additional epitopes not evaluated for immunogenicity are also included. They are an additional B7-supermotif-bearing epitope and two HLA-A1 and one HLA-A24 high-affinity binding peptides. A known HLA-A31 restricted epitope (VGIYLLPNR; SEQ ID NO:3587), which also binds HLA-A33, is also set out in Table XXXVIa and is useful in combination with other Class I or Class II epitopes.

Paragraph beginning at line 1 of page 99 (TABLE III), has been amended as follows:

TABLE III

		POSITION									
MOTIFS		1° anchor 1	2	3	4	5	1° anchor 6	7	8	9	
DR4	preferred	FMY*LIVW*	M	T		I	VST*CPALIM*	MH		MH	
	deleterious				W			R		WDE	
DR1	preferred	MF*LIVWY*			PAMQ		VMAT*SPLIC*	M		AVM	
	deleterious		C	CH	FD	CWD		GDE	D		
DR7	preferred	MF*LIVWY*	M	W	A		IVMSA*CTPL*	M		IV	(SEQ ID NO:3682)
	deleterious		C		G			GRD	N	G	(SEQ ID NO:3683)
DR Supermotif		MF*LIVWY*					VMSTA*CPLI*				

DR3 MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6
motif a preferred	LIVMFY			D		
motif b preferred	LIVMFAY			DNQEST		KRH

Italicized residues indicate less preferred or "tolerated" residues.